

## POPULATION / COMMUNITY GENETICS

*Abstracts*

### HOST GENOTYPE MAY INFLUENCE MISODENDRACEAE INFECTIONS

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In southern Argentina and Chile southern beech trees (*Nothofagus*) are infected by the endemic mistletoe *Misodendrum*. Infection intensity varies both within an individual host and at the population level, where patches of infected and non-infected trees are patchily distributed. Allozyme molecular markers were used to examine genetic differences between infected and non-infected trees at three field sites. Non-metric multidimensional scaling (NMDS) ordination was performed on the genotypes of 166 *Nothofagus antarctica* individuals (77 infected and 89 non-infected) using allele counts at 12 loci. The three field sites are distinguished in the ordination space. Two sites had a higher degree of infection of *Misodendrum punctulatum* and are in the same direction as the vector for this variable. The number of infections per tree is significantly correlated with both ordination axis. An analysis of similarity (ANOSIM) showed significant differences in genotype between infected and non-infected trees, but only for one of the two species of *Misodendrum* found on this host. The two sites with a higher degree of infection by *M. punctulatum* were not different, but were statistically distinguished from the third site. Allozyme variation may be due to infection of *M. punctulatum*, but other factors that influence the probability of being infected (such as differences in the morphotype of the host) may also contribute to the differences found. Thus, the genotype of the host does not confer resistance to Misodendraceae, but different morphotypes may increase or decrease the chance of being infected.

Keywords: *infection*, *Misodendrum*, *mistletoe*, *host genotype*.

### FIRE MANAGEMENT AND THE EFFECTS OF DRIFT AND GENE FLOW ON THE EASTERN COLLARED LIZARD, CROTAPHYTUS COLLARIS COLLARIS

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Eastern collared lizards, *Crotaphytus collaris collaris*, of the Missouri Ozarks live in glades which are open, rocky habitats imbedded in a forest matrix. Recent fire suppression has degraded glades and made the forest an effective barrier to dispersal, leading to habitat destruction, fragmentation, population isolation and local extinction. Prescribed forest fires have helped to restore the habitat and natural population dynamics of glade species. This study focuses on a reintroduced population of collared lizards that has been subjected to ten years of habitat fragmentation due to fire suppression followed by ten years of habitat restoration due to prescribed burns. Genetic, demographic, and mark-recapture data have been collected throughout the history of this population. This unique data set allows us to document the effects of genetic drift and gene flow on the genetic diversity of this population over time. Preliminary results have been generated using microsatellite markers. Prior to the initiation of prescribed

burns, results indicate low gene flow among glades as well as a decline in genetic diversity. For the years following these burns, we begin to see increased gene flow and a rise in genetic diversity. These data highlight the importance of landscape level habitat restoration for maintaining the genetic integrity of populations.

Keywords: *Population Genetics, Conservation, Fragmentation, Restoration*

INCORPORATING POPULATION GENETICS IN ECOLOGICAL MODELING: A  
METHODOLOGY FOR OBTAINING RESISTANCE VALUES IN SUBURBAN POPULATIONS OF  
*RANA SYLVATICA*

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The use of traditional null-hypothesis testing in ecological and evolutionary studies has faced numerous critiques in recent years. Model selection based upon information theoretic methods is becoming more prevalent in the literature; however, one major shortcoming of many ecological models is to overlook the inclusion of parameters based on the basic principles of population genetics. Here, I propose a methodology for obtaining reliable quantitative values for the conventional ecological concept of landscape resistance. How much a particular habitat impedes the physical movement of the animal is an important conservation issue and genetics can help tweak ecological models in potentially favourable ways. Specifying the movement and replacement/local extinction rate of individuals in each population throughout a landscape matrix is difficult at best, even with substantial empirical information on life-history patterns, behaviour, landscape connectivity, cover, etc. My study focuses on populations of wood frogs (*Rana sylvatica*) in heavily suburbanized South-Central Ontario. Wood frogs are an ideal study species because of life-history traits and suburban landscapes represent a high level of fragmentation, and potentially, resistance. Microsatellite markers will be used to help retrospectively reconstruct the physical movement processes of wood frog populations, from samples collected during the breeding season (mid March-mid April). Though still in the development phase, I will address different potential movement models developed *a priori* to sampling, with parameters of dispersal, migration, gene flow, effective population size, and assortative mating.

Keywords: *modeling, genetics, resistance, wood frog*

ANOTHER FISH, ANOTHER TALE: GENETIC STRUCTURE OF SMALLMOUTH BASS,  
*MICROPTERUS DOLOMIEU*, IN LAKE ERIE

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Mitochondrial DNA sequences, control region and cytochrome b, and 8 microsatellite nDNA loci were analyzed to investigate the genetic structure of smallmouth bass (*Micropterus dolomieu*) in Lake Erie. Population divergences were estimated using  $\mu_{ST}$  for mtDNA and two estimates from microsatellites,  $\mu_{ST}$  and  $\mu_{ST}$ , to detect population structure. Secondly, genetic covariation was partitioned hierarchically at three levels: among 3 basins in Lake Erie, among sites within basins, and within sites. Finally, overall genetic similarity among the 11 sampling sites was illustrated using minimum spanning trees. mtDNA and microsatellite data sets were corroborative in concluding that smallmouth bass populations were characterized by low population divergences.

Geographically distant sites were most frequently identified as statistically divergent. The majority of genetic variation occurred within sampling sites, but the western basin of Lake Erie was genetically divergent from the central and eastern basins allowing for hypothesis testing that Lake Erie bathymetry has contributed to population structure. Low population divergences were reflected in poorly resolved minimum spanning trees although MST of cytochrome b identified 4 groups; most notably the Bass Islands were separated from adjacent sites within the western basin. The overall population structure from these analyses suggested two potential sources of population divergence: (1) isolation by distance and subsequent reduced gene flow which is supported by field data of tagged bass and (2) reproductive isolation due to philopatry of spawning males. The latter was manifested in higher genetic divergences of geographically neighboring sites in the western basin although not statistically significant. These two factors operate at two geographical scales in Lake Erie, but neither explanation considered historical effects. Alternatively, multiple refugial populations mixing in Lake Erie following deglaciation can account for a pattern of isolation by distance. Further sampling throughout the Great Lakes and identification of glacial refugia will lead to a more robust conclusion. Regardless, it appears that the genetic variation and distribution is due potentially to a combination of historical and behavioral factors. Delineation of genetically identifiable demes will assist resource managers in a more efficient and biologically appropriate programme to conserve and sustain various stocks of this fishery.

Keywords: *smallmouth bass*, *mtDNA*, *microsatellites*, *genetic structure*

#### POPULATION GENETICS OF THE ENDANGERED ILLINOIS CAVE AMPHIPOD, *GAMMARUS ACHERONDYTES* (GAMMARIDAE)

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Limited resources and socioeconomic factors force conservation personnel to prioritize which populations of endangered taxa receive protection. The concepts of evolutionary significant units (ESUs) and management units (MUs) have been incorporated into management strategies in an attempt to develop guidelines to prioritize populations. Although the techniques used to identify these conservation units are still debated, the overall goal is to protect and maintain the genetic viability and evolutionary potential of the species. *Gammarus acherondytes* is a federally endangered species of troglobitic amphipod endemic to two hydrologically separate karst subregions (Waterloo and Renault) in southwestern Illinois. To assess genetic relationships among amphipods, the mitochondrial cytochrome c oxidase subunit I (COI) gene was sequenced from 80 individuals collected from 9 caves in the two subregions. A total of 11 unique haplotypes were identified: 5 from Waterloo, 6 from Renault. Variability among haplotypes was low (0.2 – 1.2%), and several haplotypes were found in multiple caves. However, no haplotypes were shared between subregions. Geographic structuring of haplotypes suggests that subregions are genetically isolated populations and should be managed as separate units.

Keywords: *mitochondrial DNA*, *evolutionary significant unit*, *Gammarus acherondytes*, *conservation genetics*